AMENDMENTS TO THE SPECIFICATION

Please amend the paragraph beginning at page 42, line 10, as follows:

Profile hidden Markov models are statistical models which also represent the consensus of a family of sequences. Krogh and colleagues (Krogh, A., Brown, M., Mian, I.S., Sjolander, K. and Haussler, D. 1994. Hidden Markov models in computational biology: Applications to protein modeling. *J. Mol Biol.* 235:1501-1531) applied HMM techniques to modeling sequence profiles, adopting techniques from speech recognition studies (Rabiner, L.R. 1989. A tutorial on hidden Markov models and selected applications to speech recognition. *Proc. IEEE* 77:257-286). The use of hidden Markov models for analysis of biological sequences is now well known in the art and applications for hidden Markov model calculation are readily available; for example, the program HMMER ~~(http://hmmer.wustl.edu)~~ (hmmer.wustl.edu).

Please amend the paragraph beginning at page 60, line 15, as follows:

In still another embodiment, the siRNAs are evaluated for binding specificity. See WO 01/05935 for an exemplary method of determining binding specificity of a 21mer. In a preferred embodiment, the binding specificity is evaluated by calculating a 21mer minimax score against the set of unique sequence representatives of genes of an organism, e.g., the set of unique sequences representatives for each cluster of Homo sapiens Unigene build 161 ~~(http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=unigene)~~ (ncbi.nlm.nih.gov/entrez/query.fcgi?db=unigene).

LAW OFFICES OF
CHRISTENSEN O'CONNOR JOHNSON KINDNESS^{PLLC}
1420 Fifth Avenue
Suite 2800
Seattle, Washington 98101
206.682.8100